

I CLAIM:

1. A binary composition for detecting one or more target nucleic acid sequences comprising:

a probe comprising a target-specific portion for sequence-specific hybridization to a target nucleic acid sequence, and a tag; and

a mobility-modifier comprising a tail and a tag complement for binding to the tag.

2. The composition of **claim 1** wherein the target-specific portion comprises polynucleotide.

3. The composition of **claim 2** wherein the target-specific portion comprises a 3'-hydroxyl group.

4. The composition of **claim 2** wherein the target-specific portion comprises PNA.

5. The composition of **claim 1** wherein the tag portion comprises polynucleotide.

6. The composition of **claim 5** wherein the tag portion is PNA.

~~7.6.1~~ The composition of **claim 1** wherein the tag complement portion is PNA

8. The composition of claim 1 wherein both the tag and tag complement are polynucleotide, and one of the tag complement and tag comprises a sequence selected from the group consisting of (CAG)_n and (TCC)_n wherein n is 1 to 10.

9 ~~8.~~ The composition of claim 1 wherein the mobility modifier comprises a tail portion.

10 ~~9~~. The composition of **claim 8** wherein the tail is a polymer.

11 ~~10~~. The composition of **claim 9** wherein the polymer is selected from the group consisting of polyethyleneoxide and polypeptide.

12 ~~11~~. The composition of claim 1 further comprising a hybridization enhancer.

13 ~~12~~. A method for detecting one or more target nucleic acid sequences present in a sample comprising:

5 providing a sample potentially containing one or more target nucleic acid sequences;
providing one or more probes, each probe comprising a target-specific portion and a tag;

providing one or more mobility-modifiers, each mobility modifier comprising a tag complement and a tail;

10 contacting the probe(s) and the target nucleic acid sequence(s) under conditions effective for sequence-dependent hybridization of the probe(s) and the target nucleic acid sequence(s), thereby forming a bound probe(s);

treating the bound probe(s) to form a modified probe(s);

15 contacting the probe(s), the bound probe(s) or the modified probe(s) and the mobility-modifier(s) under conditions suitable for selectively binding the tag(s) and the tag complement(s), thereby forming one or more a probe/mobility modifier complex(s); and

analyzing the probe/mobility modifier complex(s) using a mobility-dependent analysis technique under conditions that do not disrupt the probe/mobility modifier complex.

20 14 ~~13~~. The method of claim 12 wherein the step of treating the bound probe comprises a ligation reaction.

25 15 ~~14~~. The method of claim 12 wherein the step of treating the bound probe comprises a primer extension reaction.

16 ~~15~~. The method of claim 12 wherein the step of treating the bound probe comprises attaching a label to the probe.

30 17 ~~16~~. The method of claim 12 wherein the target-specific portion comprises polynucleotide.

18 17. The method of claim 16 wherein the target-specific portion comprises a 3'-hydroxyl group.

19 18. The method of claim 16 wherein the target-specific portion comprises PNA.

20 19. The method of claim 12 wherein the tag complement portion comprises polynucleotide.

21 20. The method of claim 19 wherein the tag complement portion is PNA.

22 21. The method of claim 12 wherein both the tag and tag complement are polynucleotide, and one of the tag complement and tag comprises the sequence (CAG)_n wherein n is 1 to 10.

23 22. The method of claim 12 wherein the tail is a polymer.

24 23. The method of claim 22 wherein the polymer is selected from the group consisting of polyethyleneoxide and polypeptide.

25 24. The method of claim 12 further comprising a hybridization enhancer.

26 25. The method of claim 12 wherein two or more probes and two or more mobility modifiers are provided such that each probe selectively binds to a mobility modifier, thereby forming a probe/mobility modifier complex, wherein at least two of the probe/mobility modifier complexes are resolvable in the mobility-dependent analysis technique.